



SEQUENCE LISTING

<110> Lipton, Stuart A.
Okamoto, Shu-ichi

<120> Methods of Differentiating and
Protecting Cells By Modulating the P38/MEF2 Pathway

<130> 66654-622

<140> US 09/876,187

<141> 2001-06-05

<150> US 60/209,539

<151> 2000-06-05

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<213> Homo sapiens

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1
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Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala Tyr
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Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys Asp	
85 90 95	
agc cca gac cct gat act tca tat gtg cta act cca cat aca gaa gaa	753
Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu Glu	
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aaa tat aaa aaa att aat gag gaa ttt gat aat atg atg cgg aat cat	801
Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn His	
115 120 125	
aaa atc gca cct ggt ctg cca cct cag aac ttt tca atg tct gtc aca	849
Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val Thr	
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gtt cca gtg acc agc ccc aat gct ttg tcc tac act aac cca ggg agt	897
Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly Ser	
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tca ctg gtg tcc cca tct ttg gca gcc agc tca acg tta aca gat tca	945
Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp Ser	
165 170 175	
agc atg ctc tct cca cct caa acc aca tta cat aga aat gtg tct cct	993
Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser Pro	
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Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met Leu	
195 200 205	
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Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro Val	
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Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly Ala	
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Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro Pro	
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Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp Leu	
260 265 270	
cga gtt gtc atc ccc cct tca agc aag ggc atg atg cct cca cta tcg	1281
Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu Ser	
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gcc act caa cct ctt gct acc cca gtc gtg tct gtg aca acc cca agc	1377
Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro Ser	
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Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr Asn	
325 330 335	
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Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly Phe	
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Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln Gln	
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cac cac cta gga caa gca gcc ctc agc tct ctt gtt gct gga ggg cag	1569
His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly Gln	
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tta tct cag ggt tcc aat tta tcc att aat acc aac caa aac atc agc	1617
Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile Ser	
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atc aag tcc gaa ccg att tca cct cct cgg gat cgt atg acc cca tcg	1665
Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro Ser	
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Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Tyr	
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Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro Ile	
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Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser Val	
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aag cga atg agg atg gac gcg tgg gtg acc taaggcttcc aagctgatgt	1955
Lys Arg Met Arg Met Asp Ala Trp Val Thr	
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Tyr	Glu	Leu	Ser	Val	Leu	Cys	Asp	Cys	Glu	Ile	Ala	Leu	Ile	Ile	Phe
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Asn	Ser	Ser	Asn	Lys	Leu	Phe	Gln	Tyr	Ala	Ser	Thr	Asp	Met	Asp	Lys
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Asn	Ser	Asp	Ile	Val	Glu	Ala	Leu	Asn	Lys	Lys	Glu	His	Arg	Gly	Cys
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Asp	Ser	Pro	Asp	Pro	Asp	Thr	Ser	Tyr	Val	Leu	Thr	Pro	His	Thr	Glu
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Glu	Lys	Tyr	Lys	Lys	Ile	Asn	Glu	Glu	Phe	Asp	Asn	Met	Met	Arg	Asn
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Pro	Gly	Ala	Pro	Gln	Arg	Pro	Pro	Ser	Thr	Gly	Asn	Ala	Gly	Gly	Met
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Val	Gly	Asn	Gly	Phe	Val	Asn	Ser	Arg	Ala	Ser	Pro	Asn	Leu	Ile	Gly
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Ala	Thr	Gly	Ala	Asn	Ser	Leu	Gly	Lys	Val	Met	Pro	Thr	Lys	Ser	Pro
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Ser Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser					
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Gln Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro					
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Ser Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr					
	325		330		335
Asn Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly					
	340		345		350
Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln					
	355		360		365
Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly					
	370		375		380
Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile					
385		390		395	400
Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro					
	405		410		415
Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro					
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Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln					
	435		440		445
Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser					
	450		455		460
Tyr Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro					
465		470		475	480
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 tcattccact cagcctggga cg atg ggg agg aaa aaa atc cag atc tcc cgc 472
 Met Gly Arg Lys Lys Ile Gln Ile Ser Arg
 1 5 10
 atc ctg gac caa agg aat cgg cag gtg acg ttc acc aag cgg aag ttc 520
 Ile Leu Asp Gln Arg Asn Arg Gln Val Thr Phe Thr Lys Arg Lys Phe
 15 20 25

ggg ctg atg aag aag gcc tat gag ctg agc gtg ctc tgt gac tgt gag	568
Gly Leu Met Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu	
30 35 40	
ata gcc ctc atc atc ttc aac agc gcc aac cgc ctc ttc cag tat gcc	616
Ile Ala Leu Ile Ile Phe Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala	
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agc acg gac atg gac cgt gtg ctg ctg aag tac aca gag tac agc gag	664
Ser Thr Asp Met Asp Arg Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu	
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ccc cac gag agc cgc acc aac act gac atc ctc gag acg ctg aag cgg	712
Pro His Glu Ser Arg Thr Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg	
75 80 85 90	
agg ggc att ggc ctc gat ggg cca gag ctg gag ccg gat gaa ggg cct	760
Arg Gly Ile Gly Leu Asp Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro	
95 100 105	
gag gag cca gga gag aag ttt cgg agg ctg gca ggc gaa ggg ggt gat	808
Glu Glu Pro Gly Glu Lys Phe Arg Arg Leu Ala Gly Glu Gly Gly Asp	
110 115 120	
ccg gcc ttg ccc cga ccc cgg ctg tat cct gca gct cct gct atg ccc	856
Pro Ala Leu Pro Arg Pro Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro	
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Ser Pro Asp Val Val Tyr Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro	
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agt ggg ctt ggg gaa gca ctg ccc gcc cag agc cgc cca tct ccc ttc	952
Ser Gly Leu Gly Glu Ala Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe	
155 160 165 170	
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Arg Pro Ala Ala Pro Lys Ala Gly Pro Pro Gly Leu Val His Pro Leu	
175 180 185	
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205 210 215	
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ctg agc gcc tct ctc cgg ccc ccg ggg gcc ccg gcg act ttc cta aga 1336
Leu Ser Ala Ser Leu Arg Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg
                285                290                295

cct tcc cct atc cct tgc tcc tcg ccc ggt ccc tgg cag agc ctc tgc 1384
Pro Ser Pro Ile Pro Cys Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys
                300                305                310

ggc ctg ggc ccg ccc tgc gcc ggc tgc cct tgg ccg acg gct ggc ccc 1432
Gly Leu Gly Pro Pro Cys Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro
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ggt agg aga tca ccc ggt ggc acc agc cca gag cgc tcg cca ggt acg 1480
Gly Arg Arg Ser Pro Gly Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr
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gcg agg gca cgt ggg gac ccc acc tcc ctc cag gcc tct tca gag aag 1528
Ala Arg Ala Arg Gly Asp Pro Thr Ser Leu Gln Ala Ser Ser Glu Lys
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acc caa cag tgacgcccc ctccgcggtg ggggcttgga ggtgggcggc 1577
Thr Gln Gln
                365

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<210> 4

<211> 365

<212> PRT

<213> Homo sapiens

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Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Arg
 50          55          60
Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr
 65          70          75          80
Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg Arg Gly Ile Gly Leu Asp
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Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro Glu Glu Pro Gly Glu Lys
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Phe Arg Arg Leu Ala Gly Glu Gly Gly Asp Pro Ala Leu Pro Arg Pro
115         120         125

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		180						185					190		
Thr	Ser	Lys	Thr	Pro	Pro	Pro	Leu	Tyr	Leu	Pro	Thr	Glu	Gly	Arg	Arg
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Ser	Asp	Leu	Pro	Gly	Gly	Leu	Ala	Gly	Pro	Arg	Gly	Gly	Leu	Asn	Thr
210					215						220				
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Gly	Thr	Ser	Pro	Glu	Arg	Ser	Pro	Gly	Thr	Ala	Arg	Ala	Arg	Gly	Asp
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 Met Gly Arg Lys Lys
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att cag att acg agg att atg gat gaa cgt aac aga cag gtg aca ttt 464
 Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn Arg Gln Val Thr Phe
 10 15 20

aca aag agg aaa ttt ggg ttg atg aag aag gct tat gag ctg agc gtg 512

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Leu	Cys	Asp	Cys	Glu	Ile	Ala	Leu	Ile	Ile	Phe	Asn	Ser	Thr	Asn	Lys		
		40					45					50					
ctg	ttc	cag	tat	gcc	agc	acc	gac	atg	gac	aaa	gtg	ctt	ctc	aag	tac	608	
Leu	Phe	Gln	Tyr	Ala	Ser	Thr	Asp	Met	Asp	Lys	Val	Leu	Leu	Lys	Tyr		
	55					60					65						
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Thr	Glu	Tyr	Asn	Glu	Pro	His	Glu	Ser	Arg	Thr	Asn	Ser	Asp	Ile	Val		
	70				75					80					85		
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Gly Tyr Pro Ser Ala Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser Leu	
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Ile Lys Ser Glu Pro Val Ser Pro Pro Arg Asp Arg Thr Thr Thr Pro	
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Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
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Gly	Ser	Asp	Arg	Glu	Asp	His	Arg	Asn	Glu	Phe	His	Ser	Pro	Ile	Gly	
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Leu	Thr	Arg	Pro	Ser	Pro	Asp	Glu	Arg	Glu	Ser	Pro	Ser	Val	Lys	Arg	
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<210> 7

<211> 1919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<400> 7

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Met Gly Arg Lys Lys Ile Gln Ile Gln Arg Ile Thr
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Asp Glu Arg Asn Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu
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atg aag aag gcg tat gag ctg agc gtg cta tgt gac tgc gag atc gca 327
Met Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala
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Asp Met Asp Lys Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His
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Glu Ser Arg Thr Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly
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Phe Asn Gly Cys Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu
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Gln Ser Pro Leu Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu
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Ser Tyr Glu Thr Gly Asp Arg Asp Asp Gly Arg Gly Asp Phe Gly Pro			
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